Predicting Stroke

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Importing dataset and necessary libraries

```
stroke <- read.csv("c:/Users/steph/OneDrive/Documents/USD/ADS503/healthcare-dataset-stroke-data.csv")
```

```
library(caret) # for training models
library(e1071)
library(Hmisc)
library(corrplot)
library(plyr)
library(pROC)
```

```
str(stroke)
```

```
## 'data.frame':    5110 obs. of  12 variables:
##  $ id               : int  9046 51676 31112 60182 1665 56669 53882 10434 27419 60491 ...
##  $ gender           : chr  "Male" "Female" "Male" "Female" ...
##  $ age              : num  67 61 80 49 79 81 74 69 59 78 ...
##  $ hypertension     : int  0 0 0 0 1 0 1 0 0 0 ...
##  $ heart_disease    : int  1 0 1 0 0 0 1 0 0 0 ...
##  $ ever_married     : chr  "Yes" "Yes" "Yes" "Yes" ...
##  $ work_type        : chr  "Private" "Self-employed" "Private" "Private" ...
##  $ Residence_type   : chr  "Urban" "Rural" "Rural" "Urban" ...
##  $ avg_glucose_level: num  229 202 106 171 174 ...
##  $ bmi              : chr  "36.6" "N/A" "32.5" "34.4" ...
##  $ smoking_status   : chr  "formerly smoked" "never smoked" "never smoked" "smokes" ...
##  $ stroke           : int  1 1 1 1 1 1 1 1 1 1 ...
```

Many of the categorical variables are characters – we will need to change those to factors.

```
dim(stroke)
```

```
## [1] 5110   12
```

There are 5110 observations, with 12 features, including the target variable.

```
# changing datatypes to what they should be
stroke$hypertension <- as.factor(stroke$hypertension)
stroke$heart_disease <- as.factor(stroke$heart_disease)
```

```
stroke$gender <- as.factor(stroke$gender)
stroke$ever_married <- as.factor(stroke$ever_married)
stroke$work_type <- as.factor(stroke$work_type)
stroke$Residence_type <- as.factor(stroke$Residence_type)
stroke$smoking_status <- as.factor(stroke$smoking_status)
stroke$bmi <- as.numeric(stroke$bmi)
stroke$stroke <- as.factor(stroke$stroke)
```

```
# checking nulls
colSums(is.na(stroke))
```

```
##                id            gender               age      hypertension
##                 0                 0                 0                 0
##     heart_disease      ever_married         work_type    Residence_type
##                 0                 0                 0                 0
## avg_glucose_level               bmi    smoking_status            stroke
##                 0               201                 0                 0
```

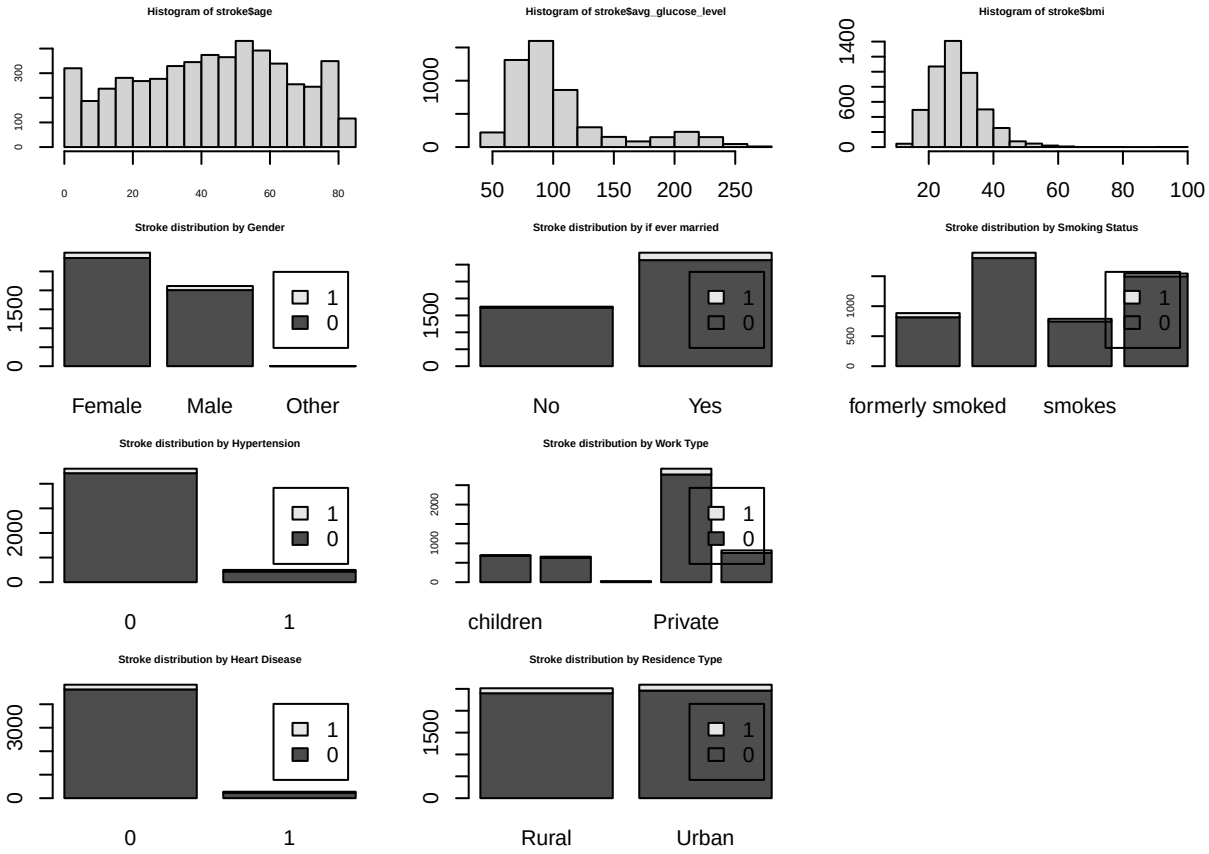
There are 201 nulls in BMI.

```
summary(stroke)
```

```
##        id           gender          age        hypertension heart_disease
##  Min.   :   67   Female:2994   Min.   : 0.08   0:4612       0:4834
##  1st Qu.:17741   Male  :2115   1st Qu.:25.00   1: 498       1: 276
##  Median :36932   Other :   1   Median :45.00
##  Mean   :36518                 Mean   :43.23
##  3rd Qu.:54682                 3rd Qu.:61.00
##  Max.   :72940                 Max.   :82.00
##
##  ever_married         work_type    Residence_type avg_glucose_level
##  No :1757     children     : 687   Rural:2514     Min.   : 55.12
##  Yes:3353     Govt_job     : 657   Urban:2596     1st Qu.: 77.25
##               Never_worked :  22                  Median : 91.89
##               Private      :2925                  Mean   :106.15
##               Self-employed: 819                  3rd Qu.:114.09
##                                                   Max.   :271.74
##
##       bmi                smoking_status stroke
##  Min.   :10.30   formerly smoked: 885   0:4861
##  1st Qu.:23.50   never smoked   :1892   1: 249
##  Median :28.10   smokes         : 789
##  Mean   :28.89   Unknown        :1544
##  3rd Qu.:33.10
##  Max.   :97.60
##  NA's   :201
```

1 “other” gender. 1544 “unknown” smoker status. 201 nulls in BMI. Work type “Private” means what? Any cutoff for minimum Age? Target variable Stroke seems pretty imbalanced.

```r
# plots for all features
par(mar = c(2,2,2,2))
layout.matrix <- matrix(c(1,4,5,6,2,7,8,9,3,10,0,0),nrow = 4, ncol = 3)

layout(mat = layout.matrix,
       heights = c(4, 4, 4, 4),
       widths = c(3, 3, 3))
# histogram for numerical features
hist(stroke$age, cex.main = .5, cex.axis = .5)
hist(stroke$avg_glucose_level, cex.main = .5)
hist(stroke$bmi, cex.main = .5)

# bar charts for categorical
countGen <- table(stroke$stroke,stroke$gender)
barplot(countGen, main = "Stroke distribution by Gender", legend = rownames(countGen), cex.lab = .5, ce

countHyp <- table(stroke$stroke, stroke$hypertension)
barplot(countHyp, main = "Stroke distribution by Hypertension", legend = rownames(countHyp), cex.lab= .

countHd <- table(stroke$stroke,stroke$heart_disease)
barplot(countHd, main = "Stroke distribution by Heart Disease", legend = rownames(countHd), cex.lab = .

countMarried <- table(stroke$stroke, stroke$ever_married)
barplot(countMarried, main = "Stroke distribution by if ever married", legend = rownames(countMarried),

countWork <- table(stroke$stroke, stroke$work_type)
barplot(countWork, main = "Stroke distribution by Work Type", legend = rownames(countWork), cex.lab = .

countRes <- table(stroke$stroke, stroke$Residence_type)
barplot(countRes, main = "Stroke distribution by Residence Type", legend = rownames(countRes), cex.lab =

countSmoke <- table(stroke$stroke, stroke$smoking_status)
barplot(countSmoke, main = "Stroke distribution by Smoking Status", legend = rownames(countSmoke), cex.
```




```
# glucose levels look skewed slightly, as does bmi numbers
# let's check for skewness
skewness(stroke$avg_glucose_level)
```

```
## [1] 1.571361
```

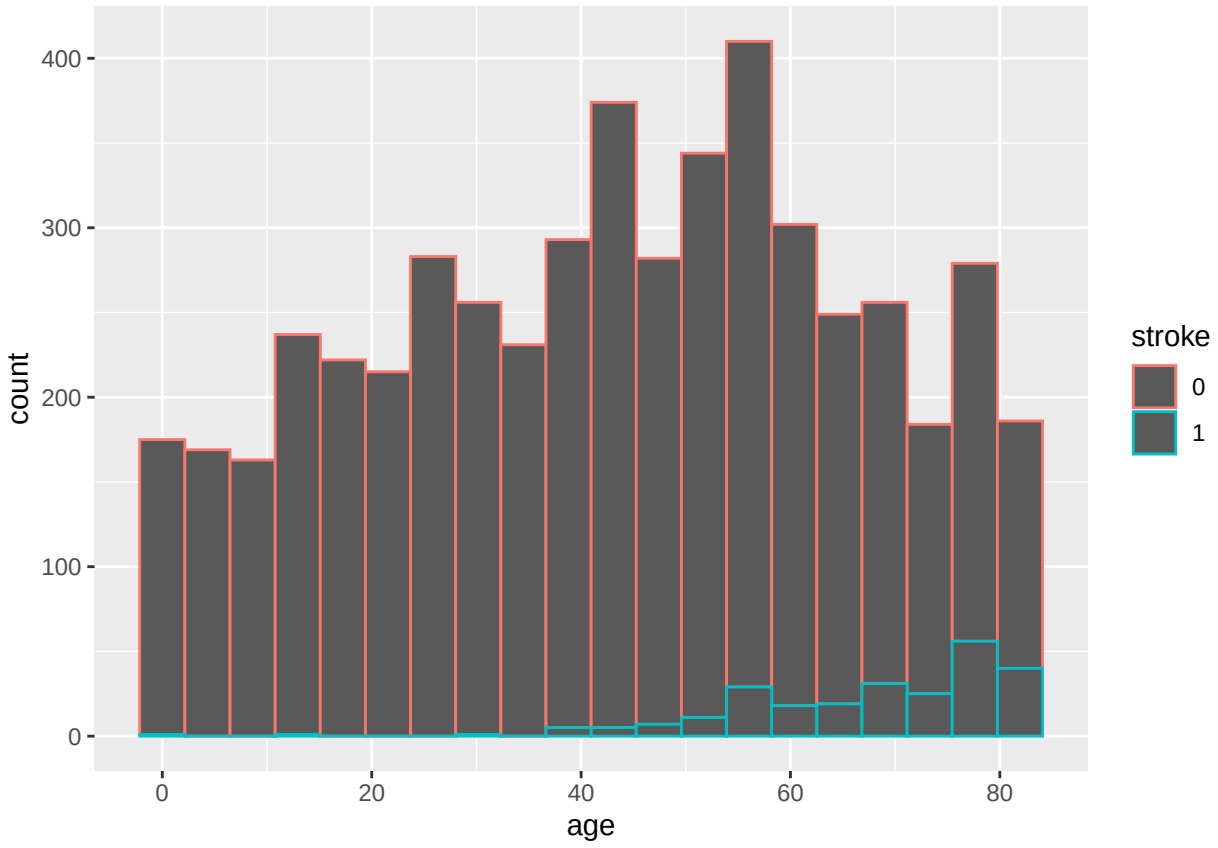
```
skewness(stroke$bmi) ## need to get rid of nulls to see skewness metric
```

```
## [1] NA
```

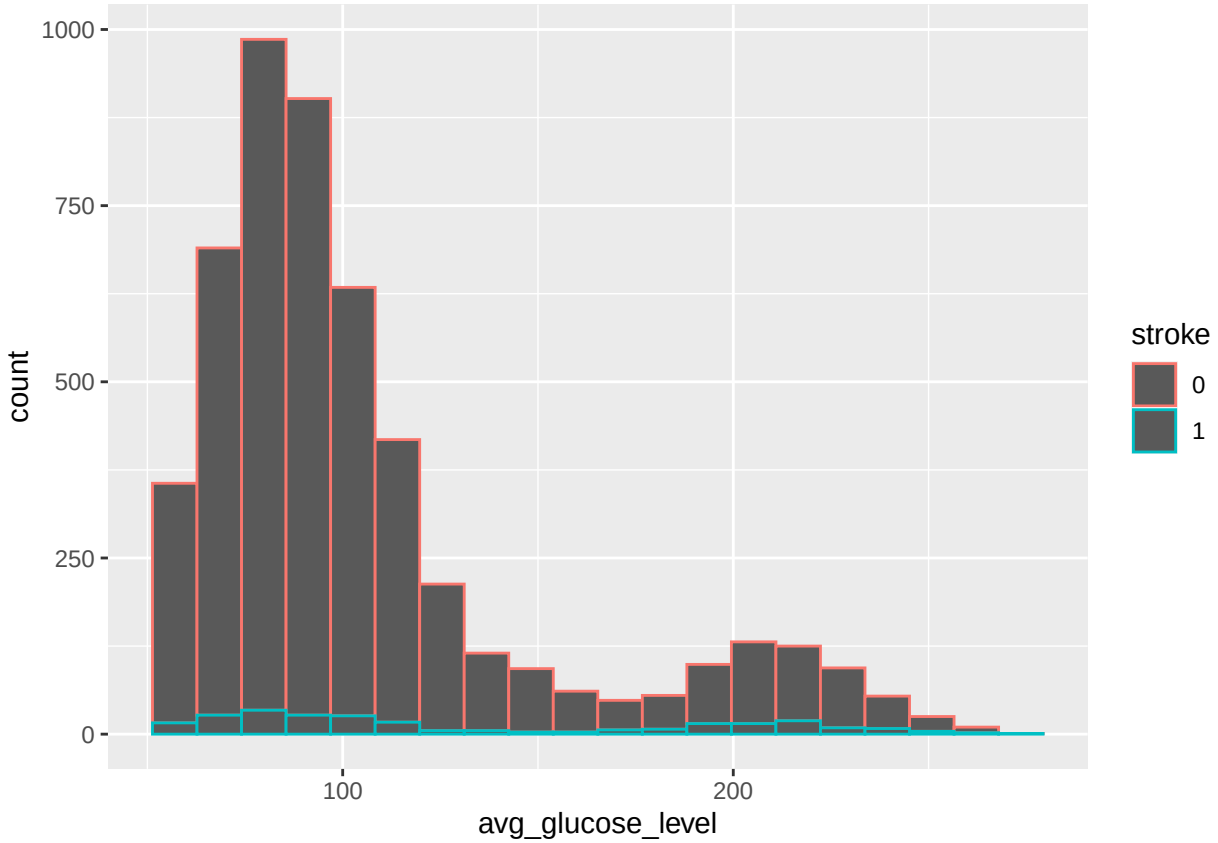
```
skewness(stroke$age)
```

```
## [1] -0.1369789
```

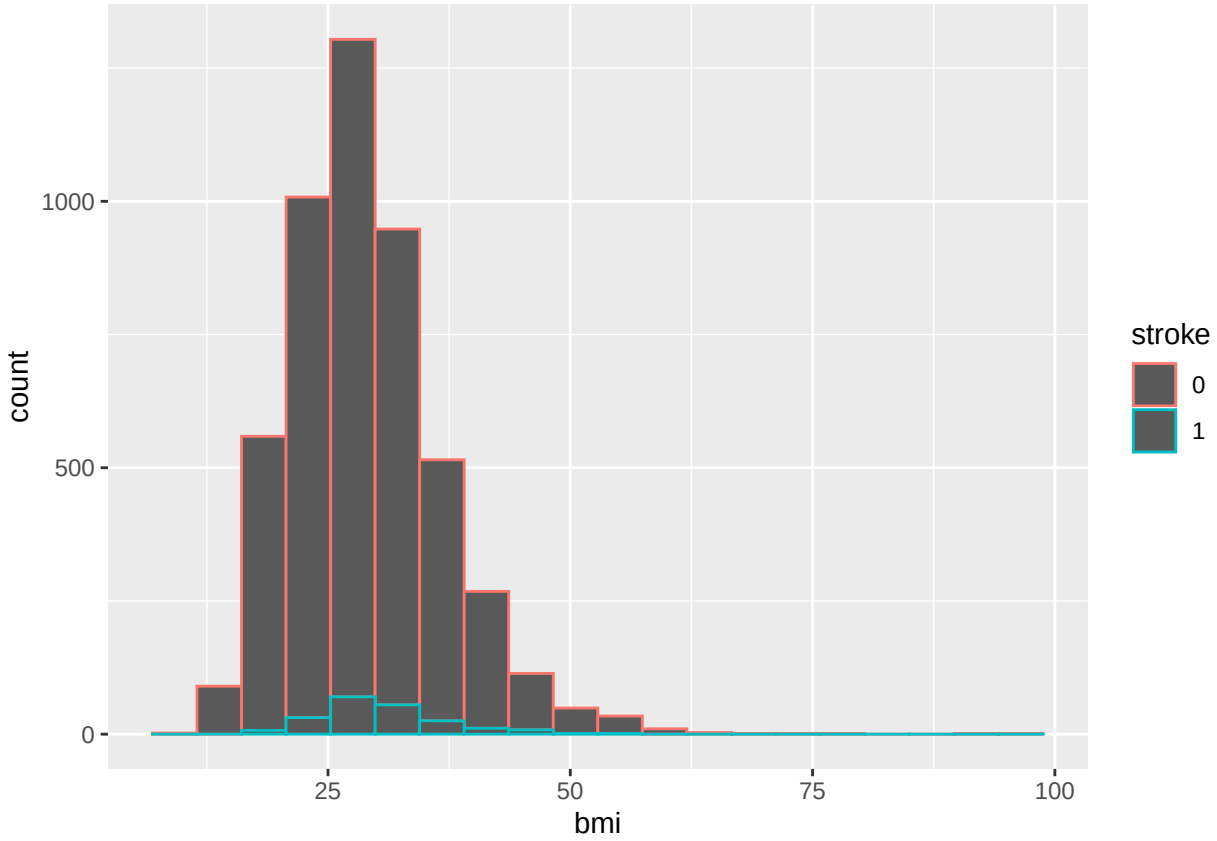
```
# let's investigate the numeric variables further
ggplot(stroke, aes(x=age,color=stroke)) + geom_histogram(bins = 20)
```




```
ggplot(stroke, aes(x=avg_glucose_level,color=stroke)) + geom_histogram(bins = 20)
```




```
ggplot(stroke, aes(x=bmi,color=stroke)) + geom_histogram(bins = 20)
```


count
1000
500
0
25
50
75
100
bmi
stroke
0
1